

SEQUENCE LISTING

<110> E.I. du Pont de Nemours and Company, Inc.
Huang, Lixuan
Xue, Zhixiong

<120> DNA and Amino Acid Sequences of a Tyrosine Ammonia Lyase Enzyme
from the Bacterium Rhodobacter sphaeroides

<130> CL2169 US NA

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<170> PatentIn version 3.2

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<213> T. cutaneum

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Lys Val Gly Asp Val Val Ala Val Ala Arg His Gly Ala Lys Val Glu
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Leu Ala Ala Ser Val Ala Gly Pro Val Arg Ala Ser Val Asp Phe Lys
65 70 75 80

Glu Ser Lys Lys His Thr Ser Ile Tyr Gly Val Thr Thr Gly Phe Gly
85 90 95

Gly Ser Ala Asp Thr Arg Thr Ser Asp Thr Glu Ala Leu Gln Ile Ser
100 105 110

Leu Leu Glu His Gln Leu Cys Gly Phe Leu Pro Thr Asp Ala Thr Tyr
115 120 125

Glu Gly Met Leu Leu Ala Ala Met Pro Ile Pro Ile Val Arg Gly Ala
130 135 140

Met Ala Val Arg Val Asn Ser Cys Val Arg Gly His Ser Gly Val Arg
145 150 155 160

Leu Glu Val Leu Gln Ser Phe Ala Asp Phe Ile Asn Arg Gly Leu Val
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Pro Cys Val Pro Leu Arg Gly Thr Ile Ser Ala Ser Gly Asp Leu Ser
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Pro Leu Ser Tyr Ile Ala Gly Ala Ile Cys Gly His Pro Asp Val Lys
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 Val Phe Asp Thr Ala Ala Ser Pro Pro Thr Val Leu Thr Ser Pro Glu
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 Ala Ile Ala Lys Tyr Gly Leu Lys Thr Val Lys Leu Ala Ser Lys Glu
 225 230 235 240
 Gly Leu Gly Leu Val Asn Gly Thr Ala Val Ser Ala Ala Ala Gly Ala
 245 250 255
 Leu Ala Leu Tyr Asp Ala Glu Cys Leu Ala Ile Met Ser Gln Thr Asn
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 Thr Val Leu Thr Val Glu Ala Leu Asp Gly His Val Gly Ser Phe Ala
 275 280 285
 Pro Phe Ile Gln Glu Ile Arg Pro His Ala Gly Gln Ile Glu Ala Ala
 290 295 300
 Arg Asn Ile Arg His Met Leu Gly Gly Ser Lys Leu Ala Val His Glu
 305 310 315 320
 Glu Ser Glu Leu Leu Ala Asp Gln Asp Ala Gly Ile Leu Arg Gln Asp
 325 330 335
 Arg Tyr Ala Leu Arg Thr Ser Ala Gln Trp Ile Gly Pro Gln Leu Glu
 340 345 350
 Ala Leu Gly Leu Ala Arg Gln Gln Ile Glu Thr Glu Leu Asn Ser Thr
 355 360 365
 Thr Asp Asn Pro Leu Ile Asp Val Glu Gly Gly Met Phe His His Gly
 370 375 380
 Gly Asn Phe Gln Ala Met Ala Val Thr Ser Ala Met Asp Ser Ala Arg
 385 390 395 400
 Ile Val Leu Gln Asn Leu Gly Lys Leu Ser Phe Ala Gln Val Thr Glu
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 Leu Ile Asn Cys Glu Met Asn His Gly Leu Pro Ser Asn Leu Ala Gly
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 Ser Glu Pro Ser Thr Asn Tyr His Cys Lys Gly Leu Asp Ile His Cys
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 Gly Ala Tyr Cys Ala Glu Leu Gly Phe Leu Ala Asn Pro Met Ser Asn
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His Val Gln Ser Thr Glu Met His Asn Gln Ser Val Asn Ser Met Ala
 465 470 475 480
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 485 490 495
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 Val Met Glu Val Lys Phe Lys Met Ala Ile Val Lys Leu Leu Asn Glu
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 Lys Leu Asn Thr His Ala Ala Ile Thr Leu Tyr Lys Arg Leu Asn Gln
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 Thr Pro Ser Trp Asp Ser Ala Pro Arg Phe Glu Asp Ala Ala Lys His
 565 570 575
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 580 585 590
 Asp Leu Thr Asn Leu Pro Lys Trp Lys Lys Glu Phe Ala Lys Glu Ala
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 Gly Asn Leu Tyr Arg Ser Ile Leu Val Ala Thr Thr Ala Asp Gly Arg
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 Asn Asp Leu Glu Pro Ala Glu Tyr Leu Gly Gln Thr Arg Ala Val Tyr
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 Glu Ala Val Arg Ser Glu Leu Gly Val Lys Val Arg Arg Gly Asp Val
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 35 40 45
 Glu Ala Arg Leu Gly Ala Val Ile Arg Glu Ala Arg His Val Tyr Gly
 50 55 60
 Leu Thr Thr Gly Phe Gly Pro Leu Ala Asn Arg Leu Ile Ser Gly Glu
 65 70 75 80
 Asn Val Arg Thr Leu Gln Ala Asn Leu Val His His Leu Ala Ser Gly
 85 90 95
 Val Gly Pro Val Leu Asp Trp Thr Thr Ala Arg Ala Met Val Leu Ala
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 Arg Leu Val Ser Ile Ala Gln Gly Ala Ser Gly Ala Ser Glu Gly Thr
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 Ile Ala Arg Leu Ile Asp Leu Leu Asn Ser Glu Leu Ala Pro Ala Val
 130 135 140
 Pro Ser Arg Gly Thr Val Gly Ala Ser Gly Asp Leu Thr Pro Leu Ala
 145 150 155 160
 His Met Val Leu Cys Leu Gln Gly Arg Gly Asp Phe Leu Asp Arg Asp
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 Gly Thr Arg Leu Asp Gly Ala Glu Gly Leu Arg Arg Gly Arg Leu Gln
 180 185 190
 Pro Leu Asp Leu Ser His Arg Asp Ala Leu Ala Leu Val Asn Gly Thr
 195 200 205
 Ser Ala Met Thr Gly Ile Ala Leu Val Asn Ala His Ala Cys Arg His
 210 215 220
 Leu Gly Asn Trp Ala Val Ala Leu Thr Ala Leu Leu Ala Glu Cys Leu
 225 230 235 240
 Arg Gly Arg Thr Glu Ala Trp Ala Ala Ala Leu Ser Asp Leu Arg Pro
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 His Pro Gly Gln Lys Asp Ala Ala Ala Arg Leu Arg Ala Arg Val Asp
 260 265 270
 Gly Ser Ala Arg Val Val Arg His Val Ile Ala Glu Arg Arg Leu Asp
 275 280 285

Ala Gly Asp Ile Gly Thr Glu Pro Glu Ala Gly Gln Asp Ala Tyr Ser
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Leu Arg Cys Ala Pro Gln Val Leu Gly Ala Gly Phe Asp Thr Leu Ala
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Trp His Asp Arg Val Leu Thr Ile Glu Leu Asn Ala Val Thr Asp Asn
325 330 335

Pro Val Phe Pro Pro Asp Gly Ser Val Pro Ala Leu His Gly Gly Asn
340 345 350

Phe Met Gly Gln His Val Ala Leu Thr Ser Asp Ala Leu Ala Thr Ala
355 360 365

Val Thr Val Leu Ala Gly Leu Ala Glu Arg Gln Ile Ala Arg Leu Thr
370 375 380

Asp Glu Arg Leu Asn Arg Gly Leu Pro Pro Phe Leu His Arg Gly Pro
385 390 395 400

Ala Gly Leu Asn Ser Gly Phe Met Gly Ala Gln Val Thr Ala Thr Ala
405 410 415

Leu Leu Ala Glu Met Arg Ala Thr Gly Pro Ala Ser Ile His Ser Ile
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Ser Thr Asn Ala Ala Asn Gln Asp Val Val Ser Leu Gly Thr Ile Ala
435 440 445

Ala Arg Leu Cys Arg Glu Lys Ile Asp Arg Trp Ala Glu Ile Leu Ala
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Ile Leu Ala Leu Cys Leu Ala Gln Ala Ala Glu Leu Arg Cys Gly Ser
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Gly Leu Asp Gly Val Ser Pro Ala Gly Lys Lys Leu Val Gln Ala Leu
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